

Day : Tuesday  
Date: 11/8/2005


**PALM INTRANET**

Time: 17:17:59

**Inventor Name Search Result**

Your Search was:

Last Name = TCHISTIAKOVA

First Name = LIOUDMILA

Application#	Patent#	Status	Date Filed	Title	Inventor Name
<u>09775743</u>	<u>6733755</u>	150	02/02/2001	LIGAND FOR VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR	TCHISTIAKOVA, LIOUDMILA
<u>09848537</u>	<u>6696274</u>	150	05/03/2001	LIGAND FOR ENHANCING ORAL AND CNS DELIVERY OF BIOLOGICAL AGENTS	TCHISTIAKOVA, LIOUDMILA
<u>10784589</u>	Not Issued	30	02/23/2004	Ligand for vascular endothelial growth factor receptor	TCHISTIAKOVA, LIOUDMILA
<u>11149309</u>	Not Issued	19	06/09/2005	Antibodies against human interleukin-13 and uses therefor	TCHISTIAKOVA, LIOUDMILA
<u>11155843</u>	Not Issued	19	06/17/2005	IL-13 binding agents	TCHISTIAKOVA, LIOUDMILA
<u>11221902</u>	Not Issued	19	09/09/2005	Humanized anti-5T4 antibodies and anti- 5T4/calicheamicin conjugates	TCHISTIAKOVA, LIOUDMILA
<u>60180568</u>	Not Issued	159	02/04/2000	Vascular endothelial growth factor receptor	TCHISTIAKOVA, LIOUDMILA
<u>60201981</u>	Not Issued	159	05/03/2000	Ligand for enhancing oral and CNS delivery of biological agents	TCHISTIAKOVA, LIOUDMILA
<u>60578473</u>	Not Issued	159	06/09/2004	Antibodies against human interleukin-13 and uses therefor	TCHISTIAKOVA, LIOUDMILA
<u>60581078</u>	Not Issued	159	06/17/2004	IL-13 binding antibodies	TCHISTIAKOVA, LIOUDMILA

<u>60581375</u>	Not Issued	159	06/22/2004	Antibodies against human interleukin-13 and uses therefor	TCHISTIAKOVA, LIOUDMILA
<u>60608494</u>	Not Issued	159	09/10/2004	Humanized anti-5T4 antibodies and anti- 5T4/calicheamicin conjugates	TCHISTIAKOVA, LIOUDMILA

**Inventor Search Completed:** No Records to Display.

**Search Another: Inventor**

Last Name	First Name	
<input type="text" value="tchistiakova"/>	<input type="text" value="lioudmila"/>	<input type="button" value="Search"/>

To go back use Back button on your browser toolbar.

Back to [PALM](#) | [ASSIGNMENT](#) | [OASIS](#) | [Home page](#)

OM protein - protein search, using sw model

Run on: October 13, 2005, 02:04:31 ; Search time 165 Seconds  
(without alignments)  
37.504 Million cell updates/sec

Title: US-10-784-589-7  
Perfect score: 48  
Sequence: 1 NXXEIEXXXWXXXXXY 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	30	62.5		16	4	AAU07817	Aau07817 Peptide i
4	30	62.5		16	4	AAU07822	Aau07822 Peptide i
5	29	60.4		16	4	AAU07804	Aau07804 Peptide #
6	29	60.4		16	4	AAU07818	Aau07818 Peptide i
7	29	60.4		16	4	AAU07820	Aau07820 Peptide i
8	29	60.4		16	4	AAU07811	Aau07811 Peptide i
9	29	60.4		16	4	AAU07801	Aau07801 Peptide #

10	29	60.4	17	4	AAU07803	Aau07803	Peptide #
11	29	60.4	17	4	AAU07802	Aau07802	Peptide #
12	29	60.4	19	4	AAU07805	Aau07805	Peptide #
13	28	58.3	16	4	AAU07807	Aau07807	Peptide #
14	28	58.3	106	5	ABP39180	Abp39180	Staphyloc
15	28	58.3	106	8	ADS06536	Ads06536	Staphyloc
16	27	56.2	71	4	ABB16872	Abb16872	Human ner
17	27	56.2	152	5	ABB47424	Abb47424	Listeria
18	27	56.2	183	5	ABP64176	Abp64176	Human ORF
19	27	56.2	190	7	ADH87742	Adh87742	Enterococ
20	27	56.2	194	4	ABB63149	Abb63149	Drosophil
21	27	56.2	226	5	ABB72343	Abb72343	Murine pr
22	27	56.2	294	7	ADC32653	Adc32653	Human nov
23	27	56.2	345	8	ADS24202	Ads24202	Bacterial
24	27	56.2	352	5	AAU99395	Aau99395	Human nuc
25	27	56.2	352	6	AAG79681	Aag79681	Human ENZ
26	27	56.2	995	4	ABG11717	Abg11717	Novel hum
27	27	56.2	1024	5	ABB05595	Abb05595	Human nuc
28	27	56.2	1024	7	ADJ69675	Adj69675	Human hea
29	26	54.2	16	4	AAU07823	Aau07823	Peptide i
30	26	54.2	97	5	ABP33908	Abp33908	Human ORF
31	26	54.2	148	3	AAG47498	Aag47498	Arabidops
32	26	54.2	148	3	AAG36580	Aag36580	Arabidops
33	26	54.2	150	7	ADE31116	Ade31116	Human dia
34	26	54.2	199	3	AAG19731	Aag19731	Arabidops
35	26	54.2	203	3	AAG36579	Aag36579	Arabidops
36	26	54.2	220	7	ADF04669	Adf04669	Bacterial
37	26	54.2	233	3	AAG47497	Aag47497	Arabidops
38	26	54.2	242	3	AAG30771	Aag30771	Arabidops
39	26	54.2	244	3	AAG33122	Aag33122	Zea mays
40	26	54.2	246	8	ADQ65496	Adq65496	Novel hum
41	26	54.2	247	4	ABB50249	Abb50249	Human tra
42	26	54.2	251	3	AAG19730	Aag19730	Arabidops
43	26	54.2	257	3	AAG31376	Aag31376	Arabidops
44	26	54.2	261	3	AAG36578	Aag36578	Arabidops
45	26	54.2	281	3	AAG30770	Aag30770	Arabidops

#### ALIGNMENTS

##### RESULT 1

AAU07816

ID AAU07816 standard; peptide; 16 AA.

XX

AC AAU07816;

XX

DT 07-NOV-2001 (first entry)

XX

DE Peptide insert sequence #6 relating to VEGF receptor-1 peptide ligands.

XX

KW Vascular endothelial growth factor receptor-1; VEGF; psoriasis;  
KW angiogenesis mediated disease; birth control; neovascularisation;  
KW inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;  
KW anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;  
KW anti ulcer; osteopathic; cytostatic; anti inflammatory; ophthalmological;  
KW dermatological.

OM protein - protein search, using sw model

Run on: October 13, 2005, 01:54:55 ; Search time 41 Seconds  
(without alignments)  
29.131 Million cell updates/sec

Title: US-10-784-589-7  
Perfect score: 48  
Sequence: 1 NXXEIEXXXWXXXXXY 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	30	62.5	16	4	US-09-775-743C-19	Sequence 19, Appl
3	30	62.5	16	4	US-09-775-743C-23	Sequence 23, Appl
4	30	62.5	16	4	US-09-775-743C-24	Sequence 24, Appl
5	29	60.4	16	4	US-09-775-743C-1	Sequence 1, Appli
6	29	60.4	16	4	US-09-775-743C-4	Sequence 4, Appli
7	29	60.4	16	4	US-09-775-743C-20	Sequence 20, Appl
8	29	60.4	16	4	US-09-775-743C-22	Sequence 22, Appl
9	29	60.4	17	4	US-09-775-743C-2	Sequence 2, Appli
10	29	60.4	17	4	US-09-775-743C-3	Sequence 3, Appli
11	29	60.4	19	4	US-09-775-743C-5	Sequence 5, Appli
12	28	58.3	16	4	US-09-775-743C-7	Sequence 7, Appli
13	28	58.3	106	3	US-09-134-001C-4025	Sequence 4025, Ap
14	27	56.2	190	4	US-09-134-000C-5627	Sequence 5627, Ap
15	26	54.2	16	4	US-09-775-743C-25	Sequence 25, Appl

16	26	54.2	220	4	US-09-543-681A-4954	Sequence 4954, Ap
17	26	54.2	313	3	US-09-362-506-2	Sequence 2, Appli
18	26	54.2	521	2	US-08-721-684C-2	Sequence 2, Appli
19	26	54.2	521	2	US-09-005-970-2	Sequence 2, Appli
20	26	54.2	521	3	US-09-407-715-2	Sequence 2, Appli
21	25	52.1	13	4	US-09-775-743C-29	Sequence 29, Appl
22	25	52.1	16	4	US-09-775-743C-14	Sequence 14, Appl
23	25	52.1	75	3	US-09-111-470-11	Sequence 11, Appl
24	25	52.1	75	4	US-09-862-802A-11	Sequence 11, Appl
25	25	52.1	158	4	US-09-107-532A-5873	Sequence 5873, Ap
26	25	52.1	173	3	US-08-833-488B-31	Sequence 31, Appl
27	25	52.1	197	3	US-08-833-488B-28	Sequence 28, Appl
28	25	52.1	199	3	US-08-833-488B-14	Sequence 14, Appl
29	25	52.1	201	4	US-09-489-039A-12260	Sequence 12260, A
30	25	52.1	229	3	US-08-833-488B-24	Sequence 24, Appl
31	25	52.1	253	3	US-08-833-488B-20	Sequence 20, Appl
32	25	52.1	268	4	US-09-248-796A-19955	Sequence 19955, A
33	25	52.1	325	4	US-09-325-932A-83	Sequence 83, Appl
34	25	52.1	325	4	US-09-325-932A-201	Sequence 201, App
35	25	52.1	415	4	US-09-540-236-3097	Sequence 3097, Ap
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37	25	52.1	435	4	US-09-592-998C-10	Sequence 10, Appl
38	25	52.1	471	4	US-09-134-000C-3750	Sequence 3750, Ap
39	25	52.1	633	4	US-09-583-110-3803	Sequence 3803, Ap
40	25	52.1	650	4	US-09-107-433-3849	Sequence 3849, Ap
41	25	52.1	662	4	US-09-107-532A-5989	Sequence 5989, Ap
42	25	52.1	774	3	US-09-276-400-7	Sequence 7, Appli
43	25	52.1	774	3	US-09-448-076-7	Sequence 7, Appli
44	25	52.1	774	3	US-09-702-572-7	Sequence 7, Appli
45	25	52.1	981	4	US-09-328-352-4484	Sequence 4484, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-775-743C-18

; Sequence 18, Application US/09775743C

; Patent No. 6733755

; GENERAL INFORMATION:

; APPLICANT: Supratek Pharmaceuticals, Inc.

; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: 082181-36154

; CURRENT APPLICATION NUMBER: US/09/775,743C

; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/180,568

; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemical peptide synthesis and biosynthesis utilizing E. coli

US-09-775-743C-18

Query Match 58.3%; Score 28; DB 26; Length 106;  
Best Local Similarity 38.5%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 EIEXXXWXXXXXY 16  
||| |  
Db 77 EIENSKWASVTFY 89

Search completed: October 13, 2005, 02:13:34  
Job time : 496 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 13, 2005, 02:00:50 ; Search time 79 Seconds  
(without alignments)  
37.371 Million cell updates/sec

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and is derived by analysis of the total score distribution.

#### SUMMARIES

Result %  
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3	28	58.3	106	7	US-11-208-208-4025	Sequence 4025, Ap
4	27	56.2	194	7	US-11-097-143-16239	Sequence 16239, A
5	27	56.2	294	6	US-10-489-448-2735	Sequence 2735, Ap
6	27	56.2	352	6	US-10-990-328A-9729	Sequence 9729, Ap
7	27	56.2	995	6	US-10-450-763-42076	Sequence 42076, A
8	27	56.2	1024	1	PCT-US03-10870-1481	Sequence 1481, Ap
9	26	54.2	65	6	US-10-703-032-177710	Sequence 177710,
10	26	54.2	154	6	US-10-703-032-126045	Sequence 126045,
11	26	54.2	197	6	US-10-703-032-187958	Sequence 187958,
12	26	54.2	202	8	US-60-655-875-148776	Sequence 148776,
13	26	54.2	220	7	US-11-096-568A-868	Sequence 868, App
14	26	54.2	221	7	US-11-188-298-6869	Sequence 6869, Ap
15	26	54.2	225	6	US-10-703-032-181789	Sequence 181789,
16	26	54.2	232	7	US-11-188-298-16752	Sequence 16752, A
17	26	54.2	281	6	US-10-450-763-39940	Sequence 39940, A
18	26	54.2	307	7	US-11-188-298-7162	Sequence 7162, Ap
19	26	54.2	322	7	US-11-188-298-6611	Sequence 6611, Ap
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21	26	54.2	341	6	US-10-703-032-142192	Sequence 142192,
22	26	54.2	347	6	US-10-703-032-105855	Sequence 105855,
23	26	54.2	348	6	US-10-703-032-110336	Sequence 110336,
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40	25	52.1	276	6	US-10-450-763-34121	Sequence 34121, A
41	25	52.1	279	8	US-60-655-875-139721	Sequence 139721,
42	25	52.1	318	8	US-60-655-875-136515	Sequence 136515,
43	25	52.1	341	7	US-11-055-822-570	Sequence 570, App
44	25	52.1	341	7	US-11-055-822-574	Sequence 574, App
45	25	52.1	633	5	US-09-769-744D-118	Sequence 118, App

#### ALIGNMENTS

#### RESULT 1

US-10-902-441B-4025

; Sequence 4025, Application US/10902441B

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al



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OM protein - protein search, using sw model

Run on: October 13, 2005, 02:13:47 ; Search time 40 Seconds  
(without alignments)  
38.487 Million cell updates/sec

Title: US-10-784-589-7  
Perfect score: 48  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
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2	27	56.2	152	2	AF1485	phosphotransferase
3	27	56.2	152	2	AG1124	phosphotransferase
4	27	56.2	193	2	S22881	gonadal protein gd
5	27	56.2	272	2	T08762	hypothetical prote
6	27	56.2	598	2	T01720	hypothetical prote
7	27	56.2	659	2	C85016	hypothetical prote
8	26	54.2	107	2	AG2490	hypothetical prote
9	26	54.2	132	2	C71457	hypothetical prote
10	26	54.2	135	2	C69446	hypothetical prote
11	26	54.2	194	2	AI0082	probable modulator
12	26	54.2	274	2	H71010	hypothetical prote
13	26	54.2	305	2	B82873	conserved hypothet
14	26	54.2	305	2	E84848	probable RING zinc

15	26	54.2	307	2	I40839	phospholipase D (E
16	26	54.2	307	2	A35125	phospholipase D (E
17	26	54.2	308	2	T46026	hypothetical prote
18	26	54.2	315	2	T47971	seven in absentia-
19	26	54.2	315	2	T50562	SINA2 protein [imp
20	26	54.2	315	2	T50561	SINA1 protein [imp
21	26	54.2	318	2	I39484	phospholipase D (E
22	26	54.2	327	2	T09027	hypothetical prote
23	26	54.2	335	2	E71804	hypothetical prote
24	26	54.2	336	2	S64829	hypothetical prote
25	26	54.2	336	2	T50560	SINAH1 protein [im
26	26	54.2	368	2	A81289	hypothetical prote
27	26	54.2	489	2	H89979	hypothetical prote
28	26	54.2	505	2	C86180	hypothetical prote
29	26	54.2	512	2	S61628	hypothetical prote
30	26	54.2	551	2	S65289	hypothetical prote
31	26	54.2	551	2	S66740	probable transcrip
32	26	54.2	572	2	S69014	hypothetical prote
33	26	54.2	581	2	H70125	hypothetical prote
34	26	54.2	687	2	B64126	transposase homolo
35	26	54.2	1499	2	B59431	Rho GTPase activat
36	26	54.2	2139	2	S46404	vitellogenin - yel
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40	25	52.1	213	2	E96001	probable DNA-direc
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42	25	52.1	287	2	H64538	hypothetical prote
43	25	52.1	287	2	F71967	hypothetical prote
44	25	52.1	304	2	T22766	hypothetical prote
45	25	52.1	333	2	G71801	hypothetical prote

#### ALIGNMENTS

#### RESULT 1

AG1858

hypothetical protein all0416 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AG1858

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, M.; Ishikawa, A.; Kawashima, K.; Kimura, T.; Kishida, Y.; Kohara, M.; Matsumoto, M.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120.

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG1858

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-433 <KUR>

A;Cross-references: UNIPROT:Q8YZP1; GB:BA000019; PIDN:BAB72374.1; PID:g17129761; GSPDB:GN00179

OM protein - protein search, using sw model

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Perfect score: 82  
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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7	82	100.0	19	4	US-09-775-743C-5	Sequence 5, Appli
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11	77	93.9	16	4	US-09-775-743C-16	Sequence 16, Appl

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18	71	86.6	16	4	US-09-775-743C-26	Sequence 26, Appl
19	68	82.9	16	4	US-09-775-743C-18	Sequence 18, Appl
20	68	82.9	16	4	US-09-775-743C-21	Sequence 21, Appl
21	54	65.9	16	4	US-09-775-743C-27	Sequence 27, Appl
22	47	57.3	7	4	US-09-775-743C-28	Sequence 28, Appl
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27	43	52.4	662	4	US-09-764-246-25	Sequence 25, Appl
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#### ALIGNMENTS

##### RESULT 1

US-09-775-743C-29

; Sequence 29, Application US/09775743C

; Patent No. 6733755

; GENERAL INFORMATION:

; APPLICANT: Supratek Pharmaceuticals, Inc.

; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor

; FILE REFERENCE: 082181-36154

; CURRENT APPLICATION NUMBER: US/09/775,743C

; CURRENT FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/180,568

; PRIOR FILING DATE: 2000-02-04

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 29

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; TYPE: PRT

; ORGANISM: Artificial Sequence

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Perfect score: 82
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## ALIGNMENTS

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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#### SUMMARIES

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6	82	100.0	17	33	US-10-784-589-3	Sequence 3, Appli
7	82	100.0	19	33	US-10-784-589-5	Sequence 5, Appli
8	79	96.3	16	33	US-10-784-589-20	Sequence 20, Appl
9	77	93.9	15	33	US-10-784-589-6	Sequence 6, Appli
10	77	93.9	16	33	US-10-784-589-15	Sequence 15, Appl
11	77	93.9	16	33	US-10-784-589-16	Sequence 16, Appl
12	77	93.9	16	33	US-10-784-589-22	Sequence 22, Appl
13	76	92.7	16	33	US-10-784-589-17	Sequence 17, Appl
14	76	92.7	16	33	US-10-784-589-24	Sequence 24, Appl
15	75	91.5	16	33	US-10-784-589-25	Sequence 25, Appl
16	73	89.0	16	33	US-10-784-589-19	Sequence 19, Appl
17	72	87.8	16	33	US-10-784-589-23	Sequence 23, Appl
18	71	86.6	16	33	US-10-784-589-26	Sequence 26, Appl
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# ALIGNMENTS

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; APPLICANT: Supratek Pharmaceuticals, Inc.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 082181-36154
; CURRENT APPLICATION NUMBER: US/10/784,589
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/09/775,743
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/180,568
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Chemical peptide synthesis and biosynthesis utilizing E. coli
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US-10-784-589-29

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Best Local Similarity 100.0%; Pred. No. 0.00017;
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; APPLICANT: Supratek Pharmaceuticals, Inc.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 082181-36154
; CURRENT APPLICATION NUMBER: US/10/784,589
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/09/775,743
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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30.627 Million cell updates/sec

Title: US-10-784-589-29  
Perfect score: 82  
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 829823 seqs, 183760940 residues

Total number of hits satisfying chosen parameters: 829823

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	48	58.5	632	6	US-10-531-164-2182	Sequence 2182, Ap
2	48	58.5	632	6	US-10-531-164-2183	Sequence 2183, Ap
3	48	58.5	632	6	US-10-531-164-2184	Sequence 2184, Ap
4	48	58.5	647	6	US-10-531-164-916	Sequence 916, App
5	43	52.4	406	6	US-10-990-328A-13442	Sequence 13442, A
6	43	52.4	406	6	US-10-990-328A-13443	Sequence 13443, A
7	43	52.4	406	7	US-11-222-021-1914	Sequence 1914, Ap
8	43	52.4	406	7	US-11-222-021-1917	Sequence 1917, Ap
9	43	52.4	406	8	US-60-680-004-508	Sequence 508, App

10	43	52.4	406	8	US-60-680-004-511	Sequence 511, App
11	43	52.4	456	7	US-11-096-568A-19227	Sequence 19227, A
12	43	52.4	458	7	US-11-096-568A-19226	Sequence 19226, A
13	43	52.4	467	7	US-11-096-568A-19225	Sequence 19225, A
14	43	52.4	541	7	US-11-112-882-34	Sequence 34, Appl
15	43	52.4	541	7	US-11-146-428-75	Sequence 75, Appl
16	43	52.4	661	1	PCT-US03-33139-2	Sequence 2, Appli
17	43	52.4	661	7	US-11-222-021-1916	Sequence 1916, Ap
18	43	52.4	661	8	US-60-664-579-722	Sequence 722, App
19	43	52.4	661	8	US-60-680-004-510	Sequence 510, App
20	43	52.4	662	7	US-11-033-545-315	Sequence 315, App
21	43	52.4	669	7	US-11-198-886-6	Sequence 6, Appli
22	42.5	51.8	924	7	US-11-097-143-22359	Sequence 22359, A
23	42	51.2	332	7	US-11-031-175-10805	Sequence 10805, A
24	42	51.2	398	7	US-11-031-175-11740	Sequence 11740, A
25	42	51.2	2080	6	US-10-990-328A-12272	Sequence 12272, A
26	42	51.2	2080	7	US-11-124-367A-364	Sequence 364, App
27	42	51.2	2080	8	US-60-679-970-849	Sequence 849, App
28	42	51.2	2080	8	US-60-685-372-1216	Sequence 1216, Ap
29	42	51.2	2081	8	US-60-679-970-852	Sequence 852, App
30	42	51.2	2542	6	US-10-990-328A-12273	Sequence 12273, A
31	42	51.2	2542	7	US-11-124-367A-363	Sequence 363, App
32	42	51.2	2543	8	US-60-679-970-850	Sequence 850, App
33	42	51.2	2649	8	US-60-679-970-848	Sequence 848, App
34	42	51.2	2649	8	US-60-679-970-851	Sequence 851, App
35	42	51.2	3680	6	US-10-450-763-52467	Sequence 52467, A
36	41	50.0	98	6	US-10-703-032-180803	Sequence 180803,
37	41	50.0	192	1	PCT-US04-09510-1415	Sequence 1415, Ap
38	41	50.0	434	7	US-11-178-538-63	Sequence 63, Appl
39	41	50.0	457	8	US-60-711-491-686	Sequence 686, App
40	41	50.0	547	6	US-10-270-333A-198	Sequence 198, App
41	41	50.0	547	7	US-11-097-143-42831	Sequence 42831, A
42	41	50.0	567	7	US-11-222-021-2093	Sequence 2093, Ap
43	41	50.0	635	6	US-10-703-032-119254	Sequence 119254,
44	41	50.0	669	7	US-11-222-021-2094	Sequence 2094, Ap
45	41	50.0	674	6	US-10-940-774A-7196	Sequence 7196, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-531-164-2182

; Sequence 2182, Application US/10531164

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ghosh, Malabika  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Chen, Rui-hong  
 ; APPLICANT: Wehrman, Tom

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2005, 01:26:32 ; Search time 164 Seconds  
(without alignments)  
30.658 Million cell updates/sec

Title: US-10-784-589-29  
Perfect score: 82  
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	100.0	13	4	AAU07827	Aau07827 Peptide i
2	82	100.0	16	4	AAU07804	Aau07804 Peptide #
3	82	100.0	16	4	AAU07812	Aau07812 Peptide i
4	82	100.0	16	4	AAU07811	Aau07811 Peptide i
5	82	100.0	16	4	AAU07801	Aau07801 Peptide #
6	82	100.0	17	4	AAU07803	Aau07803 Peptide #
7	82	100.0	17	4	AAU07802	Aau07802 Peptide #
8	82	100.0	19	4	AAU07805	Aau07805 Peptide #
9	79	96.3	16	4	AAU07818	Aau07818 Peptide i

10	77	93.9	15	4	AAU07806	Aau07806	Peptide #
11	77	93.9	16	4	AAU07814	Aau07814	Peptide i
12	77	93.9	16	4	AAU07820	Aau07820	Peptide i
13	77	93.9	16	4	AAU07808	Aau07808	Peptide e
14	77	93.9	16	4	AAU07813	Aau07813	Peptide i
15	76	92.7	16	4	AAU07815	Aau07815	Peptide i
16	76	92.7	16	4	AAU07822	Aau07822	Peptide i
17	75	91.5	16	4	AAU07823	Aau07823	Peptide i
18	73	89.0	16	4	AAU07817	Aau07817	Peptide i
19	72	87.8	16	4	AAU07821	Aau07821	Peptide i
20	71	86.6	16	4	AAU07824	Aau07824	Peptide i
21	68	82.9	16	4	AAU07816	Aau07816	Peptide i
22	68	82.9	16	4	AAU07819	Aau07819	Peptide i
23	54	65.9	16	4	AAU07825	Aau07825	Peptide i
24	48	58.5	632	8	ADS11946	Ads11946	Human the
25	48	58.5	632	8	ADS11947	Ads11947	Human the
26	48	58.5	632	8	ADS11945	Ads11945	Human the
27	48	58.5	647	8	ADS10679	Ads10679	Human the
28	47	57.3	7	4	AAU07826	Aau07826	Peptide i
29	43	52.4	52	8	ABO57201	Abo57201	Human gen
30	43	52.4	82	7	ADH86156	Adh86156	Enterococ
31	43	52.4	662	4	AAE00939	Aae00939	Human 15S
32	43	52.4	662	7	ADD47873	Add47873	Human Pro
33	43	52.4	662	8	ADJ75368	Adj75368	Marker ge
34	43	52.4	662	8	ADQ91786	Adq91786	Human 15S
35	43	52.4	662	8	ADQ37894	Adq37894	Human 15-
36	43	52.4	684	5	ABB08005	Abb08005	Human lip
37	42.5	51.8	57	4	AAM30997	Aam30997	Peptide #
38	42.5	51.8	57	4	ABG52390	Abg52390	Human liv
39	42.5	51.8	57	5	ABG40399	Abg40399	Human pep
40	42.5	51.8	924	4	ABB65189	Abb65189	Drosophil
41	42	51.2	320	8	ADS30364	Ads30364	Bacterial
42	42	51.2	1237	8	ABO59715	Abo59715	Human gen
43	42	51.2	2080	8	ABM82284	Abm82284	Tumour-as
44	42	51.2	2098	7	ADG42153	Adg42153	Human bra
45	42	51.2	3234	5	ABP70132	Abp70132	Human NOV

#### ALIGNMENTS

##### RESULT 1

AAU07827

ID AAU07827 standard; peptide; 13 AA.

XX

AC AAU07827;

XX

DT 07-NOV-2001 (first entry)

XX

DE Peptide insert sequence #17 relating to VEGF receptor-1 peptide ligands.

XX

KW Vascular endothelial growth factor receptor-1; VEGF; psoriasis;

KW angiogenesis mediated disease; birth control; neovascularisation;

KW inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;

KW anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;

KW anti ulcer; osteopathic; cytostatic; anti inflammatory; ophthalmological;

KW dermatological.

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OM protein - protein search, using sw model

Run on: October 8, 2005, 01:30:18 ; Search time 39 Seconds  
(without alignments)  
32.072 Million cell updates/sec

Title: US-10-784-589-29  
Perfect score: 82  
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	44.5	54.3	152	2	G75123	hypothetical prote
2	43	52.4	618	2	T24228	hypothetical prote
3	43	52.4	662	1	A31349	arachidonate 15-li
4	43	52.4	663	2	S32825	arachidonate 12-li
5	43	52.4	864	2	JC4624	alpha-glucosidase
6	43	52.4	958	1	P1BVCC	la protein - cowpe
7	42	51.2	166	2	T34229	hypothetical prote
8	41	50.0	148	2	T49732	hypothetical prote
9	41	50.0	283	2	D72378	sugar ABC transpor
10	41	50.0	434	2	T16080	hypothetical prote
11	41	50.0	442	2	S50332	NADH2 dehydrogenas
12	41	50.0	552	2	S45886	hypothetical prote
13	41	50.0	579	2	JC7896	corazonin receptor

14	41	50.0	814	2	T33140	hypothetical prote
15	41	50.0	1661	2	T31330	head-activator bin
16	40.5	49.4	334	2	A58195	cathepsin L (EC 3.
17	40.5	49.4	516	2	G82182	probable NADH dehy
18	40	48.8	100	2	D71632	hypothetical prote
19	40	48.8	221	2	B70890	hypothetical prote
20	40	48.8	307	2	AE0962	D-serine deaminase
21	40	48.8	311	2	A65010	D-serine deaminase
22	40	48.8	333	2	T19889	hypothetical prote
23	40	48.8	370	2	S54297	protein phosphatas
24	40	48.8	422	2	T49513	gastric mucin rela
25	40	48.8	435	2	D82955	probable MFS dicar
26	40	48.8	443	2	AD3050	MFS permease [alph
27	40	48.8	477	2	H98235	probable mfs dicar
28	40	48.8	477	2	G87375	major facilitator
29	40	48.8	566	2	A83832	glycine betaine tr
30	40	48.8	650	2	B87791	protein B0207.1 [i
31	40	48.8	663	1	A35087	arachidonate 12-li
32	40	48.8	663	1	A38283	arachidonate 12-li
33	40	48.8	671	2	A56592	NADPH-ferrihemopro
34	40	48.8	941	2	T32449	hypothetical prote
35	40	48.8	966	1	P1BVBB	RNA 1a protein - b
36	40	48.8	1258	2	T40737	probable calcium-t
37	39.5	48.2	214	2	G83692	hypothetical prote
38	39.5	48.2	265	2	E86600	metal dependent hy
39	39.5	48.2	265	2	E72024	metal dependent hy
40	39	47.6	184	2	F89969	conserved hypothet
41	39	47.6	279	2	T37010	probable DNA-bindi
42	39	47.6	325	2	E69806	conserved hypothet
43	39	47.6	349	2	T15422	hypothetical prote
44	39	47.6	353	2	S37873	hypothetical prote
45	39	47.6	365	2	C97735	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

G75123

hypothetical protein PAB0535 - *Pyrococcus abyssi* (strain Orsay)

C;Species: *Pyrococcus abyssi*

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C;Accession: G75123

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome structure and evolution.

A;Reference number: A75001

A;Accession: G75123

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-152 <KAW>

A;Cross-references: UNIPROT:Q9V0J9; GB:AJ248285; GB:AL096836; NID:g5458067;

PIDN:CAB49704.1; PID:g5458215

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0535

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 8, 2005, 01:29:33 ; Search time 169 Seconds  
(without alignments)  
39.391 Million cell updates/sec

Title: US-10-784-589-29  
Perfect score: 82  
Sequence: 1 EIEWYSWVTHGMY 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	47	57.3	342	2	Q66IY2	Q66iy2 xenopus lae
2	46	56.1	49	2	Q66266	Q66266 cucumber mo
3	46	56.1	342	2	Q6DFQ7	Q6dfq7 xenopus tro
4	45	54.9	209	2	Q88T96	Q88t96 lactobacill
5	45	54.9	290	2	Q9IK76	Q9ik76 spodoptera
6	45	54.9	662	1	LOXE_MOUSE	P55249 mus musculu
7	45	54.9	662	2	Q91YW6	Q91yw6 mus musculu
8	44.5	54.3	152	2	Q9V0J9	Q9v0j9 pyrococcus
9	44	53.7	593	2	Q6AMX4	Q6amx4 desulfotale
10	43	52.4	337	2	Q6SHT7	Q6sht7 uncultured
11	43	52.4	501	2	Q7SHL0	Q7shl0 neurospora
12	43	52.4	541	2	Q6WNG7	Q6wng7 euglena gra
13	43	52.4	602	2	Q966P8	Q966p8 caenorhabdi
14	43	52.4	618	2	Q22003	Q22003 caenorhabdi
15	43	52.4	661	1	LOX1_HUMAN	P16050 homo sapien



16	43	52.4	662	1	LOXP_BOVIN	P27479	bos taurus
17	43	52.4	669	2	Q8LPY6	Q8lpy6	oryza sativ
18	43	52.4	864	1	AGLU_MUCJA	Q92442	mucor javan
19	43	52.4	958	1	V1A_CCMV	P27752	cowpea chlo
20	43	52.4	959	2	Q8BEM3	Q8bem3	cowpea chlo
21	43	52.4	959	2	Q8BEM6	Q8bem6	cowpea chlo
22	42.5	51.8	924	1	ORC1_DROME	O16810	drosophila
23	42	51.2	166	2	Q19629	Q19629	caenorhabdi
24	42	51.2	185	2	Q19092	Q19092	caenorhabdi
25	42	51.2	297	2	Q82KH0	Q82kh0	streptomyce
26	42	51.2	329	2	Q7Z139	Q7z139	caenorhabdi
27	42	51.2	414	2	Q21158	Q21158	caenorhabdi
28	42	51.2	505	2	Q7RR29	Q7rr29	plasmodium
29	42	51.2	509	2	Q6VGJ5	Q6vgj5	magnolia la
30	42	51.2	557	2	Q9N4H5	Q9n4h5	caenorhabdi
31	42	51.2	594	2	Q8III3	Q8iii3	plasmodium
32	42	51.2	635	2	Q7YM60	Q7ym60	persea amer
33	42	51.2	647	2	Q7YM57	Q7ym57	anaxagorea
34	42	51.2	670	2	Q7VZP4	Q7vzp4	bordetella
35	42	51.2	670	2	Q7W5B8	Q7w5b8	bordetella
36	42	51.2	670	2	Q7WCV0	Q7wcv0	bordetella
37	42	51.2	677	2	Q7YM52	Q7ym52	degeneria r
38	42	51.2	682	2	Q7YM50	Q7ym50	galbulimima
39	42	51.2	684	2	Q7YM48	Q7ym48	magnolia tr
40	42	51.2	684	2	Q7YM49	Q7ym49	liriodendro
41	42	51.2	731	2	Q95D45	Q95d45	liriodendro
42	42	51.2	731	2	Q95DB7	Q95db7	magnolia ma
43	42	51.2	731	2	Q95DB8	Q95db8	magnolia ma
44	42	51.2	731	2	Q95DC0	Q95dc0	magnolia de
45	42	51.2	732	2	Q95CW5	Q95cw5	magnolia el

# ALIGNMENTS

## RESULT 1

Q66IY2

ID Q66IY2 PRELIMINARY; PRT; 342 AA.  
AC Q66IY2;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE MGC84181 protein.  
GN Name=MGC84181;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 16:55:44 ON  
08 NOV 2005

L1	6081 S VASCULAR (W) ENDOTHELIAL (W) GRWOTH (W) FACTOR OR VEGF (W) REC
L2	112665 S ANGIOGENESIS
L3	3490 S L1 AND L2
L4	623363 S LIGAND
L5	286 S L3 AND L4
L6	161 DUP REM L5 (125 DUPLICATES REMOVED)
L7	0 S SOLUBE (W) RECEPTOR
L8	4012 S SOLUBLE (W) RECEPTOR
L9	51 S L1 AND L8
L10	34 S L9 AND L2

L19 238093 S LI  
L20 0 S TCHISTIAKOVA  
L21 0 S PIETRZYNSKI